A modelling framework for the simulation of signal transport within 3D structure: application for the simulation of within-tree variability in floral induction in apple trees

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Introduction

Organ development and meristem fate is partly determined by endogenous signals moving within plants. These signals (e.g. hormones, sugar…) originate from organs considered as sources (roots, leaves, seeds…) and act on meristems to trigger developmental processes such as transition toward flowering. Functional structural plant model (FSPM) are of major interest as they are based on an explicit description of plant architecture needed for simulating transports within plants. Transport or fluxes have been modeled in FSPM with a special consideration on carbon allocation (Génard et al., 2008). Approaches for simulating hormone fluxes are scarce, adapted to plant with simple architecture and usually associated with a comprehensive knowledge on the processes to be simulated (Prusinkiewicz et al., 2009); thus limiting their adaptability in various contexts. In this study, we present a generic model for simulating signal fluxes and their impact on meristem fates in complex 3D tree structure. We applied this model to the simulation of within tree variability of floral induction in the apple tree, as a first case of study. Previous experiments (Belhassine et al., 2019) showed that floral induction in meristems occurs less often in the presence of fruit whereas it is favoured by the presence of leaves. Furthermore, the influences of fruit and leaves on the floral induction of meristems depend on the distances of those organs within the tree structure. Fruit and leaves were thus assumed to be sources of inhibiting signals (possibly gibberellins from seeds) and activating signals (possibly FT protein), respectively. However, the distance at which these signals move within the structure and the relative sensitivity of the meristems to these signals are highly difficult to estimate from experimental studies, only.

Material and methods

The model uses libraries from the OpenAlea platform (Pradal et al., 2008). The model runs on 3D tree architectures coded in Multiscale Tree Graphs (MTG, Godin and Caraglio, 1999). It simulates transport of signals in both acropetal and basipetal directions and a decrease in signal quantity with the distances from the emitting sources. Making use of previous formalisms developed for carbon allocation models (Reyes et al., 2020), the decrease in signal quantity depends on the distance to the emitting source and an attenuation parameter (r) modulating the effect of distances. For r values close to 0, the signal is equally distributed among organs within the structure whereas it is transported at shorter distances when r increases. The amount of signal reaching each meristem then determines its probability to switch form a developmental stage to another This fate was determined with a sigmoidal function assuming two parameters, a transition parameter (t) and a shape parameter (v). t represents the amount of signal at which the probability of the meristem to switch to another developmental stage is equal to 50% and v represents the uncertainty in SAM fate for a given amount of signal.

The model was used for simulating within tree variability in floral induction in apple tree. Fruit were considered as sources of inhibiting signal and leaves as sources of activating signal. Both signals were combined to determine the occurrence of floral induction in each

shoot apical meristem of the tree. The model was calibrated on an original database of apple trees subjected to either leaf or fruit removal at different scales of plant organization (shoot, branch, tree) to modify the intensity of signals as well as the distances between the remaining leaves, fruit and meristems (Belhassine et al., 2019). 3D mock-ups built from digitizing data and measured floral induction in the different parts of the trees were confronted to model outputs for estimating the best combinations of parameter values. The model was validated on trees subjected both to leaf and fruit removal and to contrasted crop load conditions, testing two different functions to combine the impact of activating and inhibiting signals.

Results and Discussion

Simulations performed on simple hypothetical structures showed model consistency to simulate signal effects as well as the decrease in signal amount with distances and its distribution in branching systems. Calibrations performed on apple trees for simulating within tree variability were highly relevant (R^2>0.9 and RMSE <12%). Validations were consistent when simulations were compared to trees with contrasted crop load conditions but were of lower quality for trees subjected to both leaf and fruit removal. This is probably due to difficulties to combine the effects of inhibiting and activating signal. Analysis of parameter values give some clues about the physiological processes involved as the modelling approach allowed us to quantify the distances at which activating and inhibiting signals were transported as well as the sensitivity of the meristems to these signals when considered separately.

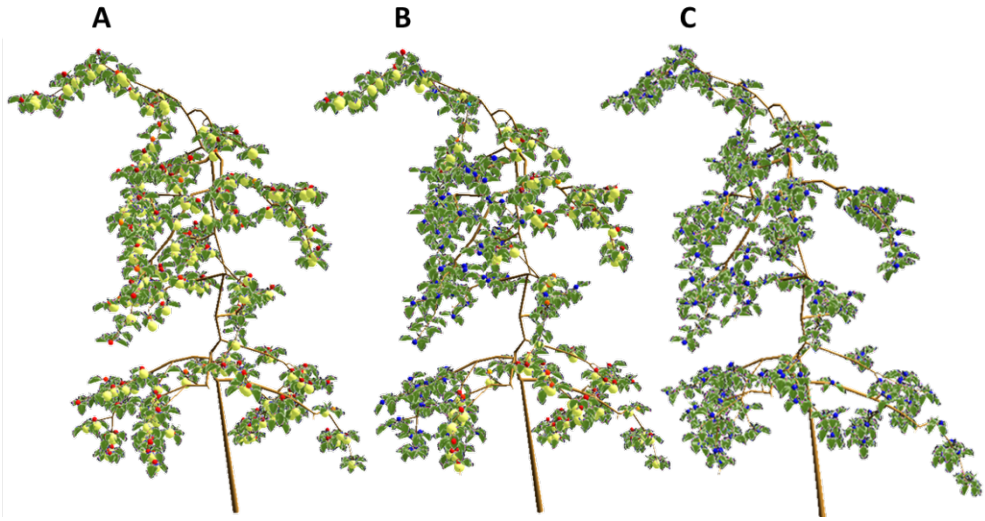

Figure: Simulation of floral induction variability in apple tree with different crop loads. A. High crop load, B. Fruit removal on half of the branches. C Low crop load (all fruit removed). Blue and red points are respectively induced and non-induced meristems.

Conclusion

The model uses MTG, a generic formalism adapted for representing all types of architectures, and simple assumptions that were compatible for simulating developmental switches such as floral induction in meristems in the apple tree case. It could be thus tested for exploring the consequences of tree architecture genetic variability on floral induction and fruiting behaviours. Experimental data are yet available and the model is currently used in this perspective.

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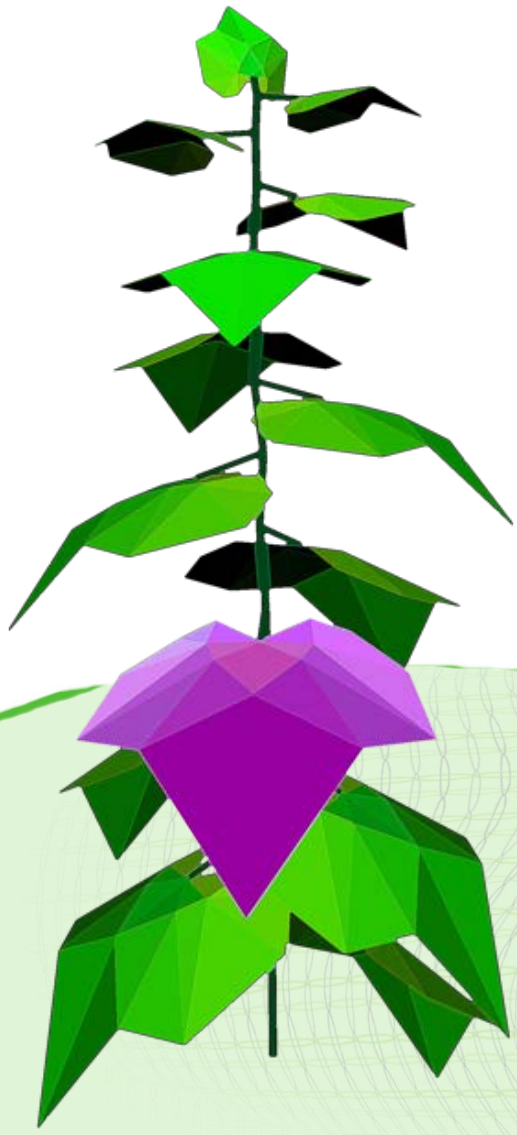

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